

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/720,896B
Source: IFW/6
Date Processed by STIC: 6/21/06

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/720,896B

DATE: 06/21/2006

TIME: 15:21:32

Input Set : A:\67452507.APP
 Output Set: N:\CRF4\06212006\J720896B.raw

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3 <110> APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
4   CHAMPION, BRIAN ROBERT
5   WARD, GEORGE ALBERT
7 <120> TITLE OF INVENTION: CONJUGATE OF A TRANSPORT PROTEIN AND A PROTEIN FOR
8   MODULATION OF NOTCH SIGNALLING
10 <130> FILE REFERENCE: 674525-2007
12 <140> CURRENT APPLICATION NUMBER: 10/720,896B
13 <141> CURRENT FILING DATE: 2003-11-24
15 <150> PRIOR APPLICATION NUMBER: PCT/GB02/02438
16 <151> PRIOR FILING DATE: 2002-05-24
18 <150> PRIOR APPLICATION NUMBER: GB 0112818.0
19 <151> PRIOR FILING DATE: 2001-05-25
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
32   for amplifying HES1 promoter from mouse genomic DNA
34 <400> SEQUENCE: 1
35 ggggtaccct caggcgccgcg ccattggcc          29
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 29
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
45   for amplifying HES1 promoter from mouse genomic DNA
47 <400> SEQUENCE: 2
48 gaagatctgc ttacgtcctt ttacttgac          29
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 26
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
58   major late promoter TATA-box motif with BglII and HindIII
59   cohesive ends
61 <400> SEQUENCE: 3
62 gatctgggg gctataaaag ggggta          26
65 <210> SEQ ID NO: 4

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: 26
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
late promoter TATA-box motif with BglII and HindIII
ve ends
CE: 4
tttatagc ccccca 26
NO: 5
: 61
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
er tetramer with XhoI and BglII cohesive ends
CE: 5
ggaaacttaa ccgtgggaac ttaaccgtgg gaacttaacc gtgggaactt 60
61
NO: 6
: 61
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
ter tetramer with XhoI and BglII cohesive ends
CE: 6
ccccacggta agttcccacg gttaagttcc cacggtaag ttcccacggt 60
61
NO: 7
I: 39
DNA
SM: Artificial Sequence
RE:
INFORMATION: Description of Artificial Sequence: Synthetic PCR
mer for generating a truncated fragment of
Notch1 cDNA
CE: 7
ccatggcacg caagcgccgg cgcaagtcat 39
NO: 8
I: 31
DNA
SM: Artificial Sequence
RE:
INFORMATION: Description of Artificial Sequence: Synthetic PCR
mer for generating a truncated fragment of
Notch1 cDNA
CE: 8
taqtccacq qqcqaqaqca t 31

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136 <210> SEQ ID NO: 9
137 <211> LENGTH: 91
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
143 annealed to the NIC2202 sequence to remove the stop codon
144 from theNIC2202 fragment of human Notch1 cDNA
146 <400> SEQUENCE: 9
147 cctggcctgt ggaagcaagg aggccaagga cctaaggca cgaggaga agtcccagga 60
148 tggcaaggggc tgccctgctgg acggcgccg c 91
151 <210> SEQ ID NO: 10
152 <211> LENGTH: 95
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
158 annealed to the NIC2202 sequence to remove the stop codon
159 from theNIC2202 fragment of human Notch1 cDNA
161 <400> SEQUENCE: 10
162 tcgagcggcc gccgtccagc aggccgcct tgccatcctg ggacttcctc ctccgtgcct 60
163 tgaggtcctt ggcctccttg cttccacagg ccagg 95
166 <210> SEQ ID NO: 11
167 <211> LENGTH: 2556
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME/KEY: MOD_RES
173 <222> LOCATION: (891)
174 <223> OTHER INFORMATION: Variable amino acid
176 <400> SEQUENCE: 11
177 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
178 1 5 10 15
180 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
181 20 25 30
183 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
184 35 40 45
186 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
187 50 55 60
189 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
190 65 70 75 80
192 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
193 85 90 95
195 Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
196 100 105 110
198 Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
199 115 120 125
201 Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
202 130 135 140
  
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204 Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
 205 145 150 155 160
 207 Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
 208 165 170 175
 210 Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
 211 180 185 190
 213 Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
 214 195 200 205
 216 Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
 217 210 215 220
 219 Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
 220 225 230 235 240
 222 His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
 223 245 250 255
 225 Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
 226 260 265 270
 228 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
 229 275 280 285
 231 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
 232 290 295 300
 234 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
 235 305 310 315 320
 237 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
 238 325 330 335
 240 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
 241 340 345 350
 243 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
 244 355 360 365
 246 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
 247 370 375 380
 249 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
 250 385 390 395 400
 252 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
 253 405 410 415
 255 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
 256 420 425 430
 258 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
 259 435 440 445
 261 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
 262 450 455 460
 264 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
 265 465 470 475 480
 267 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
 268 485 490 495
 270 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
 271 500 505 510
 273 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
 274 515 520 525
 276 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu

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| | | | |
|----------|--|-----|-----|
| 277 | 530 | 535 | 540 |
| 279 | Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly | | |
| 280 | 545 | 550 | 555 |
| 282 | Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His | | 560 |
| 283 | 565 | 570 | 575 |
| 285 | Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg | | |
| 286 | 580 | 585 | 590 |
| 288 | Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser | | |
| 289 | 595 | 600 | 605 |
| 291 | Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala | | |
| 292 | 610 | 615 | 620 |
| 294 | Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile | | |
| 295 | 625 | 630 | 635 |
| 297 | Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu | | 640 |
| 298 | 645 | 650 | 655 |
| 300 | Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly | | |
| 301 | 660 | 665 | 670 |
| 303 | Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His | | |
| 304 | 675 | 680 | 685 |
| 306 | Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys | | |
| 307 | 690 | 695 | 700 |
| 309 | Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys | | |
| 310 | 705 | 710 | 715 |
| 312 | Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly | | 720 |
| 313 | 725 | 730 | 735 |
| 315 | Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile | | |
| 316 | 740 | 745 | 750 |
| 318 | Asn Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys | | |
| 319 | 755 | 760 | 765 |
| 321 | Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser | | |
| 322 | 770 | 775 | 780 |
| 324 | Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys | | |
| 325 | 785 | 790 | 795 |
| 327 | Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn | | 800 |
| 328 | 805 | 810 | 815 |
| 330 | Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro | | |
| 331 | 820 | 825 | 830 |
| 333 | Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu | | |
| 334 | 835 | 840 | 845 |
| 336 | Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly | | |
| 337 | 850 | 855 | 860 |
| 339 | Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg | | |
| 340 | 865 | 870 | 875 |
| W--> 342 | His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys | | 880 |
| 343 | 885 | 890 | 895 |
| 345 | Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys | | |
| 346 | 900 | 905 | 910 |
| 348 | Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn | | |
| 349 | 915 | 920 | 925 |

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 891

VERIFICATION SUMMARY

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L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:880